[課程―２]

審査の結果の要旨

氏名 アクサラ　トンプラチュム

Aksara Thongprachum

Acute gastroenteritis continues to be a major public health problem worldwide. A wide variety of viruses associated with the disease are continually being reported. The accumulated surveillance data have shown that the predominant genotypes of diarrheal viruses in each epidemic season change over time. Therefore, this study aimed to investigated the epidemiological situation of diarrheal virus infections and the genetic diversity of norovirus circulating in Japanese outpatients. This study found that:

1. The surveillance identified diarrheal viruses currently circulating in Japanese pediatric outpatients in 72.1% of the Japenanse outpatients enrolled in this study. Norovirus was detected in 43.0%, followed by group A rotavirus (17.2%), human parechovirus (7.3%), enterovirus (7.0%), adenovirus (5.8%), sapovirus (5.3%), human astrovirus (2.9%), and Aichi virus (0.1%). Co-infections of diarrheal viruses were observed, with 13.4% of double infection and 0.5% of triple infection. Mixed viral infections were commonly found in Japanese outpatients, and norovirus seems to play a major role in co-infections. Viral diarrhea cases were detected mostly in children younger than 3 years of age and accounting for 72.2%. The norovirus and group A rotavirus can be detected throughout the year, with a peak during the cold and dry seasons, while other common viruses are found during no specific season.

2. Surveillance data revealed that among viruses has caused diarrhea circulating in Japanese pediatric outpatients, norovirus was found as the most important pathogens. From a total of 2,908 specimens, 43.0% of norovirus positive sample with several genotypes were detected in this study. GII.4 dominated over other genotypes (64.5%). The Den_Haag_2006b (36.9%) was detected as the predominant variant in co-circulation with New_Orleans_2009 (14.9%) until March 2012, subsequently, was displaced by the new Sydney_2012 variant. The Sydney_2012 variant has been responsible for the majority of norovirus infections since 2012 until now. Although Sydney_2012 variant has a common ancestor with New_Orleans_2009 variant, analysis of P2 subdomain showed a high level of diversity compared with other variants in four amino acid changes at the antigenic sites.

3. Analysis of the P2 subdomain also showed a high level of diversity compared with other variants in HBGA binding sites. The Sydney_2012 showed strong binding to H-active α1,2-fucosylated structures in human saliva and gastric mucosa preparations from secretor individuals irrespective of thier ABO and Lewis phenotypes, but absence of

binding specificity to Le^a-active α1,4-fucosylated structure. The expression of α1,2-fucosylated glycans seem to be crucial for susceptibility to infection of Sydney_2012 strain. However, it still remain to be investigated whether the outbreak of new genotypes with different antigenicities will result in the change of binding specificity in norovirus variants to escape from the present human immune system against norovirus infection.